



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 125858

TO: Manjunath N Rao
Location: REM-3B81/3C70
Art Unit: 1652

~~June~~ 2, 2004

July

Case Serial Number: 09/914543

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: July 1, 2004, 21:58:24 ; Search time 102 Seconds
(without alignments)
5223.067 Million cell updates/sec

Title: US-09-914-543-45

Perfect score: 960

Sequence: 1 atgagcaagaagaagtcgt.....atagaccttattcctaa 960

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	960	100.0	960	4	US-09-134-078-60
2	114.2	11.9	867	3	US-08-995-280C-1
3	53.8	5.6	7218	1	US-08-232-463-14
4	37.8	3.9	728	4	US-08-956-171E-611
5	36	3.8	936	4	US-09-636-182A-16
6	34.8	3.6	1242	4	US-09-134-000C-3076
7	34.8	3.6	3146	4	US-09-620-312D-277
8	34.8	3.6	15016	4	US-09-601-198-60
9	34.2	3.6	1161	4	US-09-328-352-1845
10	33.8	3.5	1664976	4	US-08-916-421B-1
11	33.4	3.5	3543	4	US-09-224-024-27
12	33.4	3.5	3543	5	PCT-US94-07902-27
13	33.2	3.5	612	3	US-08-385-982-400
14	32.8	3.4	832	4	US-09-621-976-2813
15	32.8	3.4	1422	1	US-08-319-704-5
16	32.4	3.4	3735	4	US-09-543-681A-2102
17	32.4	3.4	90541	4	US-09-759-359A-3
18	32.2	3.4	645	4	US-09-328-352-661
19	32	3.3	1652	4	US-09-375-140-8
20	32	3.3	11049	4	US-10-204-708-22
21	31.8	3.3	828	4	US-09-371-056-9
22	31.8	3.3	1664	4	US-09-357-787-68
23	31.8	3.3	1664	4	US-09-357-787-67
24	31.8	3.3	1892	4	US-09-276-438-12
25	31.8	3.3	4242	4	US-09-276-438-11
26	31.8	3.3	4487	4	US-09-484-970B-96
27	31.8	3.3	44453	4	US-09-146-053-5

28	31.6	3.3	480	4	US-09-621-976-8465
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31	31.6	3.3	1185	3	US-09-295-028-15
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44	31.4	3.3	261	3	US-08-906-616-160
45	31.4	3.3	261	3	US-08-639-075A-160

ALIGNMENTS

RESULT 1
US-09-134-078-60
Sequence 60, Application US/09134078
Patent No. 6168844

GENERAL INFORMATION:
APPLICANT: Bvlna, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 658/677-1456
TELEFAX: 658/677-1456

INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...957
US-09-134-078-60

Query Match 100.0%; Score 960; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 1,2e+291;

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Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	61 TATTTTGTAGAAAAAGTATCATACCTCTGAGACAAGTCAACTTAATCCTCATACACA	120
QY	CCACCCCAACCAACACTTTCACATACCAAGGTTCTCAGATTAGTATACCTCGATGACGGT	180
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QY	CCACCCCAACCAACACTTTCACATACCAAGGTTCTCAGATTAGTATACCTCGATGACGGT	180
Db	121 CCACCCCAACCAACACTTTCACATACCAAGGTTCTCAGATTAGTATACCTCGATGACGGT	180
QY	GAGTGGCCAGAGAGCTCCATTTAGTAAGATGGTATGGGAACCCAGATTCTTACATGGAA	240
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QY	ATTAACCTATAGGAACATTTCTTAATGCTATCGAATTGTCGATGATGACGTACATTTAAC	300
Db	241 ATTAACCTATAGGAACATTTCTTAATGCTATCGAATTGTCGATGATGACGTACATTTAAC	300
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Db	301 AGCGGCGTCCCTCATCAACGTCGCAACCACTTGAACAATGTGCTTGAGGGATAGAAAGTAT	360
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QY	TAGGAGACATTTTAAGTGTGAGCAACATTTACGCTTAACCAATTAACAAGAACTT	840
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RESULT 2
US-08-995-280C-1
; Sequence 1, Application US/08995280C
; Patent No. 6043075
; GENERAL INFORMATION:
; APPLICANT: Bjornvad, Mads Eskelund

1 APPLICANT: Schulein, Martin
 2 APPLICANT: No. 6043075revd, Iben Angelica
 3 TITLE OF INVENTION: A No. 6043075el Endoglucanase
 4 NUMBER OF SEQUENCES: 7
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: No. 60430750 No. 6043075disk of No. 6043075th America, Inc.
 7 STREET: 405 Lexington Avenue
 8 CITY: New York
 9 STATE: NY
 10 COUNTRY: USA
 11 ZIP: 10174
 12 COMPUTER READABLE FORM:
 13 MEDIUM TYPE: Floppy disk
 14 COMPUTER: IBM PC compatible
 15 OPERATING SYSTEM: PC-DOS/MS-DOS
 16 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 17 CURRENT APPLICATION DATA:
 18 APPLICATION NUMBER: US/08/995,280C
 19 FILING DATE: 19-Dec-1997
 20 CLASSIFICATION: 435
 21 ATTORNEY/AGENT INFORMATION:
 22 NAME: Rozek, Carol A.
 23 REGISTRATION NUMBER: 36,993
 24 REFERENCE/DOCKET NUMBER: 4906,200-US
 25 TELECOMMUNICATION INFORMATION:
 26 TELEPHONE: 212-867-0123
 27 TELEFAX: 212-878-9655
 28 TELEX:
 29 INFORMATION FOR SEQ ID NO: 1:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 867 base pairs
 32 TYPE: nucleic acid
 33 STRANDEDNESS: single
 34 TOPOLOGY: linear
 35 MOLECULE TYPE: DNA (genomic)
 36 US-08-995-280C-1

Query Match	11.9%	Score 114.2	DB 3	Length 867
Best Local Similarity	51.3%	Pred. No. 6	26	3
Matches	291	Conservative	0	Mismatches 273
			Indels	Gaps
				1
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Db	437	TGGAAACATGATACAAAGAACCCATACGAAACCG--TTACTTCAGGGGATATAG	493	
Qy	590	AAGTATGATATGGAATTACTATGACAGATTTACACACCGGCTGGCTCCAAAGTTAAGAGA	649	
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 00:46:24 ; Search time 650 Seconds
(without alignments)
7124.984 Million cell updates/sec

Title: US-09-914-543-45

Perfect score: 960
Sequence: 1 atgagcaagaaagtcgt.....atagactctattctcta 960

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	960	100.0	960 15 US-10-093-037-60	Sequence 60, Appl
3	958.4	99.8	1134 14 US-10-003-759-4	Sequence 4, Appl
4	536.8	55.9	978 15 US-10-228-063-58	Sequence 58, Appl
5	534	55.6	903 15 US-10-228-063-56	Sequence 56, Appl
6	84.2	8.8	825 16 US-10-369-493-26728	Sequence 26728, A
7	39	4.1	585 15 US-10-027-632-197533	Sequence 197533, A
8	39	4.1	585 16 US-10-027-632-197533	Sequence 197533, A
9	37.8	3.9	728 8 US-08-781-986A-611	Sequence 611, App
10	37.8	3.9	728 13 US-10-339-624-611	Sequence 611, App
11	37.2	3.9	2338 9 US-09-917-800A-1558	Sequence 1558, App
12	36.8	3.8	520 13 US-10-142-426-144	Sequence 144, App
13	36.8	3.8	520 15 US-10-123-155-144	Sequence 144, App
14	36.8	3.8	520 15 US-10-146-731-144	Sequence 144, App

ALIGNMENTS

15	36.8	3.8	520 15	US-10-140-472-144	Sequence 144, App
16	36.8	3.8	520 15	US-10-141-761-144	Sequence 144, App
17	36.8	3.8	520 15	US-10-142-885-144	Sequence 144, App
18	36.8	3.8	520 15	US-10-158-790-144	Sequence 144, App
19	36.8	3.8	520 16	US-10-137-871-144	Sequence 144, App
20	36.8	3.8	520 16	US-10-140-923-144	Sequence 144, App
21	36.8	3.8	520 16	US-10-141-756-144	Sequence 144, App
22	36.8	3.8	520 16	US-10-141-759-144	Sequence 144, App
23	36.8	3.8	520 16	US-10-140-805-144	Sequence 144, App
24	36.8	3.8	520 16	US-10-140-864-144	Sequence 144, App
25	36.6	3.8	517 13	US-10-027-632-53266	Sequence 53266, A
26	36.6	3.8	517 16	US-10-027-632-53266	Sequence 53266, A
27	36.4	3.8	741 13	US-10-076-555-659	Sequence 659, App
28	36.4	3.8	25580 9	US-09-070-927A-19	Sequence 19, Appl
29	36.2	3.8	453 13	US-10-424-599-79602	Sequence 79602, A
30	36	3.8	671 15	US-10-066-543-464	Sequence 444, App
31	36	3.8	936 15	US-10-261-845-16	Sequence 16, Appl
32	36	3.8	12393 15	US-10-311-455-1236	Sequence 1236, App
33	35.6	3.7	368 13	US-10-085-783A-21026	Sequence 21026, A
34	35.6	3.7	368 16	US-10-242-535A-21026	Sequence 21026, A
35	35.6	3.7	497 9	US-09-920-300A-1495	Sequence 1495, App
36	35.6	3.7	497 14	US-10-033-528-1495	Sequence 1495, App
37	35.6	3.7	497 15	US-10-099-926-1495	Sequence 1495, App
38	35.6	3.7	506 9	US-09-998-596-499	Sequence 499, App
39	35.6	3.7	1083 13	US-10-282-122A-17036	Sequence 17036, A
40	35.4	3.7	26747 17	US-10-240-411-20	Sequence 20, Appl
41	35.2	3.7	496 10	US-09-930-213-162	Sequence 162, App
42	35	3.6	611 13	US-10-027-632-188647	Sequence 188647, A
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44	34.8	3.6	573 10	US-09-814-353-5866	Sequence 5866, App
45	34.8	3.6	573 10	US-09-814-353-12147	Sequence 12147, A

RESULT 1

US-10-121-032-60
Sequence 60, Application US/10121032
Publication NO. US2002015550A1

GENERAL INFORMATION:

APPLICANT: Bvlin, Edward J.
TITLE OR INVENTION: GLYCOSIDASE ENZYMES

NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:

ADDRESSER: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA

COUNTRY: USA
ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/121,032
FILING DATE: 09-Apr-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/124,078
FILING DATE: 13-Aug-1998

APPLICATION NUMBER: 08/949,026
FILING DATE: 10-Oct-1997

APPLICATION NUMBER: 60/056,916
FILING DATE: 06-Dec-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Lisa A.
REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 858/677-1456

TELEFAX: 858/677-1465
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1..957
 SEQUENCE DESCRIPTION: SEQ ID NO: 60:
 US-10-121-032-60

Query Match 100.0%; Score 960; DB 14; Length 960;
 Best Local Similarity 100.0%; Pred. No. 3.4e-272;
 Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGCAGAGAAAGTTGCTGATCGTATCTTATCTTAAGCAATCCTTTAGTACAGGCATA 60
 1 ATGAGCAGAGAAAGTTGCTGATCGTATCTTATCTTAAACATCCTTTAGTACAGGCATA 60
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 61 TATTTGTGAAAGATCATACCTCTGAGACAAGTCAACTTCAATCACTCATCTCA 120
 121 CCAACCCCAACACACTTTCACACAGTTCTCAAGATTAGATACCTGATACGGT 180
 121 CCAACCCCAACACACTTTCACACAGTTCTCAAGATTAGATACCTGATACGGT 180
 181 GATGCGCAGAGACTCCTATGATAGATGAGATGAGAACCCAGAAATTTACATTGAA 240
 181 GATGCGCAGAGACTCCTATGATAGATGAGATGAGAACCCAGAAATTTACATTGAA 240
 241 ATAAACCTATGAAACATTTCTTAATGCTACTGATTTGCTGAGATGACGTAATTAAAC 300
 241 ATAAACCTATGAAACATTTCTTAATGCTACTGATTTGCTGAGATGACGTAATTAAAC 300
 301 AGGCGGCTCCTTCACTACGTCGCAACAACTTGACAACTTGTCTGAGAGATGAGATAT 360
 301 AGGCGGCTCCTTCACTACGTCGCAACAACTTGACAACTTGTCTGAGAGATGAGATAT 360
 361 TGGGTGATGATACCCCGAAATTTCTATGAAACCAAGCCTGAAATCAACTACGCA 420
 361 TGGGTGATGATACCCCGAAATTTCTATGAAACCAAGCCTGAAATCAACTACGCA 420
 421 ACTGATGCGCAATACCTATACCACTTAAGTTTCAACCTTACAGATCTTATCTTACA 480
 421 ACTGATGCGCAATACCTATACCACTTAAGTTTCAACCTTACAGATCTTATCTTACA 480
 481 ATCTCCTATAAATTGAGCCCAAGAAAGGCTGCCAATTAATCTGCAATAGAAATCTGG 540
 481 ATCTCCTATAAATTGAGCCCAAGAAAGGCTGCCAATTAATCTGCAATAGAAATCTGG 540
 541 TTAACGAGAGAGCTTGAGAGACAAAGGATTTAAAGGATGAGAGAAAGTATGATA 600
 541 TTAACGAGAGAGCTTGAGAGACAAAGGATTTAAAGGATGAGAGAAAGTATGATA 600
 601 TGAATTTACTATGACGATTAACAACCGGCTGCTCCAAAGTTAAGAGATTTGATGCCA 660
 601 TGAATTTACTATGACGATTAACAACCGGCTGCTCCAAAGTTAAGAGATTTGATGCCA 660
 661 ATAAATGTTAACGGAACACAGTAATGCTACATTTGAAGATGAGAAAGCAATTTGGT 720
 661 ATAAATGTTAACGGAACACAGTAATGCTACATTTGAAGATGAGAAAGCAATTTGGT 720
 721 TGGAGATGATGATTTAATTAAGAAACCCCAATCAAGAGGAAACAGTGAATTTCA 780
 721 TGGAGATGATGATTTAATTAAGAAACCCCAATCAAGAGGAAACAGTGAATTTCA 780
 781 TAGGAGCATTTAATAGTTTGACGCAACATTTCAAGCTTACAAATTAACAGAACTT 840
 781 TAGGAGCATTTAATAGTTTGACGCAACATTTCAAGCTTACAAATTAACAGAACTT 840

RESULT 2
 US-10-093-037-60
 Sequence 60, Application US/10093037
 Publication No. US2003078397A1
 GENERAL INFORMATION:
 APPLICANT: Jay M. Short
 APPLICANT: Byline, Edward
 APPLICANT: Swanson, Ronald V.
 APPLICANT: Mathur, Eric J.
 APPLICANT: Lam, David E.
 TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
 FILE REFERENCE: 09010-024006
 CURRENT APPLICATION NUMBER: US/10/093,037
 PRIOR APPLICATION NUMBER: US 09/910,579
 PRIOR FILING DATE: 2001-07-20
 PRIOR APPLICATION NUMBER: US 09/134,078
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 08/949,026
 PRIOR FILING DATE: 1997-10-10
 PRIOR APPLICATION NUMBER: US 60/056,916
 PRIOR FILING DATE: 1996-12-06
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 60
 LENGTH: 960
 TYPE: DNA
 ORGANISM: Pyrococcus furiosus
 US-10-093-037-60

Query Match 100.0%; Score 960; DB 15; Length 960;
 Best Local Similarity 100.0%; Pred. No. 3.4e-272;
 Matches 960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGCAGAGAAAGTTGCTGATCGTATCTTATCTTAAACATCCTTTAGTACAGGCATA 60
 1 ATGAGCAGAGAAAGTTGCTGATCGTATCTTATCTTAAACATCCTTTAGTACAGGCATA 60
 61 TATTTGTGAAAGATCATACCTCTGAGACAAGTCAACTTCAATCACTCATCTCA 120
 61 TATTTGTGAAAGATCATACCTCTGAGACAAGTCAACTTCAATCACTCATCTCA 120
 121 CCAACCCCAACACACTTTCACACAGTTCTCAAGATTAGATACCTGATACGGT 180
 121 CCAACCCCAACACACTTTCACACAGTTCTCAAGATTAGATACCTGATACGGT 180
 181 GATGCGCAGAGACTCCTATGATAGATGAGATGAGAACCCAGAAATTTACATTGAA 240
 181 GATGCGCAGAGACTCCTATGATAGATGAGATGAGAACCCAGAAATTTACATTGAA 240
 241 ATAAACCTATGAAACATTTCTTAATGCTACTGATTTGCTGAGATGACGTAATTAAAC 300
 241 ATAAACCTATGAAACATTTCTTAATGCTACTGATTTGCTGAGATGACGTAATTAAAC 300
 301 AGGCGGCTCCTTCACTACGTCGCAACAACTTGACAACTTGTCTGAGAGATGAGATAT 360
 301 AGGCGGCTCCTTCACTACGTCGCAACAACTTGACAACTTGTCTGAGAGATGAGATAT 360
 361 TGGGTGATGATACCCCGAAATTTCTATGAAACCAAGCCTGAAATCAACTACGCA 420
 361 TGGGTGATGATACCCCGAAATTTCTATGAAACCAAGCCTGAAATCAACTACGCA 420
 421 ACTGATGCGCAATACCTATACCACTTAAGTTTCAACCTTACAGATCTTATCTTACA 480

Db 421 ACTGATGGCCCAATACATTAACCAAGTAAAGTTTCAACCACTTACAGACTTCTATCTTACA 480
Qy 481 ATCTCTATTAATCTTGAAGCCCAAGAGCGCTGCCAATTAATCTTGAAGTAACTCTGG 540
Db 481 ATCTCTATTAATCTTGAAGCCCAAGAGCGCTGCCAATTAATCTTGAAGTAACTCTGG 540
Qy 541 TTACAGAGAGAGCTTGAAGAACACAGAGATTAACAGGATGAGCAAGAGTAAATGA 600
Db 541 TTACAGAGAGAGCTTGAAGAACACAGAGATTAACAGGATGAGCAAGAGTAAATGA 600
Qy 601 TGAATTTACTATGATGAGATTAACAGCGGCTGCTCAAGTTAAGAGATTTACTCTCCA 660
Db 601 TGAATTTACTATGATGAGATTAACAGCGGCTGCTCAAGTTAAGAGATTTACTCTCCA 660
Qy 661 ATAAATGTTAACCGAACACCAAGTAAATGCTACATTTGAAGTATGGAAGGCAAACTTGGT 720
Db 661 ATAAATGTTAACCGAACACCAAGTAAATGCTACATTTGAAGTATGGAAGGCAAACTTGGT 720
Qy 721 TGGGAGTATGTTGCAATTTAGAAATTAAGACCCCAATTAAGAGGAAACATGACATTTCCA 780
Db 721 TGGGAGTATGTTGCAATTTAGAAATTAAGACCCCAATTAAGAGGAAACATGACATTTCCA 780
Qy 781 TACGAGCAATTTAAGTGTGAGCCCAATTTCAAGCTTACCAATTAACAGAACTT 840
Db 781 TACGAGCAATTTAAGTGTGAGCCCAATTTCAAGCTTACCAATTAACAGAACTT 840
Qy 841 TACTTGAGAGACCTGAGAGATTTGAATGAGCTTGAAGCCCAAGCACTACCTCCGCCAC 900
Db 841 TACTTGAGAGACCTGAGAGATTTGAATGAGCTTGAAGCCCAAGCACTACCTCCGCCAC 900
Qy 901 CTGAGTGTGATGATCAAAACATPAACATTAACCTCTGATGAGAGCTTATTTCTTAA 960
Db 901 CTGAGTGTGATGATCAAAACATPAACATTAACCTCTGATGAGAGCTTATTTCTTAA 960

RESULT 3

US-10-003-759-4
; Sequence 4, Application US/10003759
; Publication No. US20020102699A1
; GENERAL INFORMATION:
; APPLICANT: Micher, Krzysztof B.
; APPLICANT: Holst, Olaf Peder
; APPLICANT: Hoechem, Maher Yousef Abou
; APPLICANT: Karlsson, Eva Margareta No. US20020102699A1dberg
; APPLICANT: Heggvidsson, Gudmundur O.
; TITLE OF INVENTION: Thermostable Cellulase
; FILE REFERENCE: P5099PC00
; CURRENT APPLICATION NUMBER: US/10/003,759
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: PCT/IS01/00012
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/594,884
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Pyrococcus furiosus
; FEATURE:
; NAME/KEY: exon
; LOCATION: (82)..(1041)
; OTHER INFORMATION:
US-10-003-759-4

Query Match 99.8%; Score 958.4; DB 14; Length 1134;
Best Local Similarity 99.9%; Pred. No. 1,1e-271;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGCAAGAAAAGTTGTCATGATCTATCTTATTAACAATCTTTAGTACAGGCAATA 60
Db 82 ATGAGCAAGAAAAGTTGTCATGATCTATCTTATTAACAATCTTTAGTACAGGCAATA 141

Qy 61 TATTTGTAGAAAAGTATGATCTGAGGACAGTCAACTTCAATTAATCTTATCTTACA 120
Db 142 TATTTGTAGAAAAGTATGATCTGAGGACAGTCAACTTCAATTAATCTTATCTTACA 201
Qy 121 CCAGCCCAACACACTTTTCCACTACCAAGTTCTGAAGTTGATTAACCTGATGACGGT 180
Db 202 CCAGCCCAACACACTTTTCCACTACCAAGTTCTGAAGTTGATTAACCTGATGACGGT 261
Qy 181 GAGTGGCAAGAGCTCTTATGATTAAGATGATGATGGAAGCCAGATTTCTACATTTGA 240
Db 262 GAGTGGCAAGAGCTCTTATGATTAAGATGATGATGGAAGCCAGATTTCTACATTTGA 321
Qy 241 ATAAACCTATGAAACATTTCTTAATGCTATGATGATTTGCTGATGATGATTTTACC 300
Db 322 ATAAACCTATGAAACATTTCTTAATGCTATGATGATTTGCTGATGATGATTTTACC 381
Qy 301 AGCGGCTCTTCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 382 AGCGGCTCTTCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 441
Qy 361 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 442 TGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 501
Qy 421 ACTGATGGCCCAATACATTAACCAAGTAAATGCTACATTTGAAGTATGGAAGGCAAT 480
Db 502 ACTGATGGCCCAATACATTAACCAAGTAAATGCTACATTTGAAGTATGGAAGGCAAT 561
Qy 481 ATCTCTATTAATCTTGAAGCCCAAGAGCGCTGCCAATTAATCTTGAAGTAACTCTGG 540
Db 562 ATCTCTATTAATCTTGAAGCCCAAGAGCGCTGCCAATTAATCTTGAAGTAACTCTGG 621
Qy 541 TTACAGAGAGAGCTTGAAGAACACAGAGATTAACAGGATGAGCAAGAGTAAATGA 600
Db 622 TTACAGAGAGAGCTTGAAGAACACAGAGATTAACAGGATGAGCAAGAGTAAATGA 681
Qy 601 TGAATTTACTATGATGAGATTAACAGCGGCTGCTCAAGTTAAGAGATTTACTCTTACA 660
Db 682 TGAATTTACTATGATGAGATTAACAGCGGCTGCTCAAGTTAAGAGATTTACTCTTACA 741
Qy 661 ATAAATGTTAACCGAACACCAAGTAAATGCTACATTTGAAGTATGGAAGGCAAACTTGGT 720
Db 742 ATAAATGTTAACCGAACACCAAGTAAATGCTACATTTGAAGTATGGAAGGCAAACTTGGT 801
Qy 721 TGGGAGTATGTTGCAATTTAGAAATTAAGACCCCAATTAAGAGGAAACATGACATTTCCA 780
Db 802 TGGGAGTATGTTGCAATTTAGAAATTAAGACCCCAATTAAGAGGAAACATGACATTTCCA 861
Qy 861 TACGAGCAATTTAAGTGTGAGCCCAATTTCAAGCTTACCAATTAACAGAACTT 921
Db 862 TACGAGCAATTTAAGTGTGAGCCCAATTTCAAGCTTACCAATTAACAGAACTT 981
Qy 841 TACTTGAGAGACCTGAGAGATTTGAATGAGCTTGAAGCCCAAGCACTACCTCCGCCAC 900
Db 922 TACTTGAGAGACCTGAGAGATTTGAATGAGCTTGAAGCCCAAGCACTACCTCCGCCAC 981
Qy 901 CTGAGTGTGATGATCAAAACATPAACATTAACCTCTGATGAGAGCTTATTTCTTAA 960
Db 982 CTGAGTGTGATGATCAAAACATPAACATTAACCTCTGATGAGAGCTTATTTCTTAA 1041

RESULT 4

US-10-228-063-58
; Sequence 58, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lianhan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109946.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60

Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSKKKVIYSILITLLVQAIFYEKKHTSEDKSTSTSTPQTLLSTTKVKIRYPDDG 60
Db 1 MSKKKVIYSILITLLVQAIFYEKKHTSEDKSTSTSTPQTLLSTTKVKIRYPDDG 60
QY 61 EMPGAPIDKGDGNPEFYIEINLMNLNATGFAEMTYNLTSGVLHYVQOLDNIVLRDRSN 120
Db 61 EMPGAPIDKGDGNPEFYIEINLMNLNATGFAEMTYNLTSGVLHYVQOLDNIVLRDRSN 120
QY 121 WHGYPEIFYGNKPMNANYATDGPILPSPKVSNLDFYLTISYKLEPKNGLPINFALBSW 180
Db 121 WHGYPEIFYGNKPMNANYATDGPILPSPKVSNLDFYLTISYKLEPKNGLPINFALBSW 180
QY 181 LTRAWRTGINSDEQEVMIWYDGLQPSGSKVKEIWPPIVNGTPVNAFEEWKANIG 240
Db 181 LTRAWRTGINSDEQEVMIWYDGLQPSGSKVKEIWPPIVNGTPVNAFEEWKANIG 240
QY 241 WEYVAFRIKTPKEGTVTIPYGAFISVANISLSLPYTELVDVEIGTEFGTPTTSAH 300
Db 241 WEYVAFRIKTPKEGTVTIPYGAFISVANISLSLPYTELVDVEIGTEFGTPTTSAH 300
QY 301 LEWMITNITLTPDRPLIS 319
Db 301 LEWMITNITLTPDRPLIS 319
```

RESULT 2
US-10-121-032-64
Sequence 64, Application US/10121032
Publication No. US20020155550A1

GENERAL INFORMATION:

APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/121,032
FILING DATE: 09-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halie, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 64:

US-10-121-032-64

Query Match 100.0%; Score 1701; DB 13; Length 319;
Best Local Similarity 100.0%; Pred. No. 7,9e-160;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSKKKVIYSILITLLVQAIFYEKKHTSEDKSTSTSTPQTLLSTTKVKIRYPDDG 60
Db 1 MSKKKVIYSILITLLVQAIFYEKKHTSEDKSTSTSTPQTLLSTTKVKIRYPDDG 60
QY 61 EMPGAPIDKGDGNPEFYIEINLMNLNATGFAEMTYNLTSGVLHYVQOLDNIVLRDRSN 120
Db 61 EMPGAPIDKGDGNPEFYIEINLMNLNATGFAEMTYNLTSGVLHYVQOLDNIVLRDRSN 120
QY 121 WHGYPEIFYGNKPMNANYATDGPILPSPKVSNLDFYLTISYKLEPKNGLPINFALBSW 180
Db 121 WHGYPEIFYGNKPMNANYATDGPILPSPKVSNLDFYLTISYKLEPKNGLPINFALBSW 180
QY 181 LTRAWRTGINSDEQEVMIWYDGLQPSGSKVKEIWPPIVNGTPVNAFEEWKANIG 240
Db 181 LTRAWRTGINSDEQEVMIWYDGLQPSGSKVKEIWPPIVNGTPVNAFEEWKANIG 240
QY 241 WEYVAFRIKTPKEGTVTIPYGAFISVANISLSLPYTELVDVEIGTEFGTPTTSAH 300
Db 241 WEYVAFRIKTPKEGTVTIPYGAFISVANISLSLPYTELVDVEIGTEFGTPTTSAH 300
QY 301 LEWMITNITLTPDRPLIS 319
Db 301 LEWMITNITLTPDRPLIS 319
```

RESULT 3
US-10-093-037-64
Sequence 64, Application US/10093037
Publication No. US20030078397A1

GENERAL INFORMATION:

APPLICANT: Jay M. Short
APPLICANT: Bylina, Edward
APPLICANT: Swanson, Ronald V.
APPLICANT: Mathur, Eric J.
APPLICANT: Lam, David B.
TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: 09010-024006
CURRENT APPLICATION NUMBER: US/10/093,037
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 09/910,579
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/056,916
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 319
TYPE: PRT
ORGANISM: *Pyrococcus furiosus*
US-10-093-037-64

Query Match 100.0%; Score 1701; DB 14; Length 319;
Best Local Similarity 100.0%; Pred. No. 7,9e-160;
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSKKKVIYSILITLLVQAIFYEKKHTSEDKSTSTSTPQTLLSTTKVKIRYPDDG 60
Db 1 MSKKKVIYSILITLLVQAIFYEKKHTSEDKSTSTSTPQTLLSTTKVKIRYPDDG 60
QY 61 EMPGAPIDKGDGNPEFYIEINLMNLNATGFAEMTYNLTSGVLHYVQOLDNIVLRDRSN 120
Db 61 EMPGAPIDKGDGNPEFYIEINLMNLNATGFAEMTYNLTSGVLHYVQOLDNIVLRDRSN 120
QY 121 WHGYPEIFYGNKPMNANYATDGPILPSPKVSNLDFYLTISYKLEPKNGLPINFALBSW 180
Db 121 WHGYPEIFYGNKPMNANYATDGPILPSPKVSNLDFYLTISYKLEPKNGLPINFALBSW 180
QY 181 LTRAWRTGINSDEQEVMIWYDGLQPSGSKVKEIWPPIVNGTPVNAFEEWKANIG 240
Db 181 LTRAWRTGINSDEQEVMIWYDGLQPSGSKVKEIWPPIVNGTPVNAFEEWKANIG 240
QY 241 WEYVAFRIKTPKEGTVTIPYGAFISVANISLSLPYTELVDVEIGTEFGTPTTSAH 300
Db 241 WEYVAFRIKTPKEGTVTIPYGAFISVANISLSLPYTELVDVEIGTEFGTPTTSAH 300
QY 301 LEWMITNITLTPDRPLIS 319
Db 301 LEWMITNITLTPDRPLIS 319
```

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Page 3

QY 121 WVGPEIFGKPKMNNAYATDGPILPSKYSNLTDFLTSTYKLEPKNGLPINFALESW 180
DB 121 WVGPEIFGKPKMNNAYATDGPILPSKYSNLTDFLTSTYKLEPKNGLPINFALESW 180
QY 181 LTRBAMRTTGINSDEOEVMWIIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIG 240
DB 181 LTRBAMRTTGINSDEOEVMWIIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIG 240
QY 241 WEYAFRIKTPKIGETVTIPYGAFTSVANATSSLPNTYELVEVEIGTEGPTSTSAH 300
DB 241 WEYAFRIKTPKIGETVTIPYGAFTSVANATSSLPNTYELVEVEIGTEGPTSTSAH 300
QY 301 LEWMTNTITLTPDRPLIS 319
DB 301 LEWMTNTITLTPDRPLIS 319

RESULT 4

US-10-228-063-55
Sequence 55, Application US/10228063
Publication No. US2003013585A1
GENERAL INFORMATION:
APPLICANT: Lananan, Mike
TITLE OF INVENTION: Self-Processing Plants and Plant Parts
FILE REFERENCE: 109846.317
CURRENT APPLICATION NUMBER: US/10/228,063
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 300
TYPE: PR1
ORGANISM: Pyrococcus furiosus
US-10-228-063-55

Query Match 95.1%; Score 1617; DB 14; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 IYFVKKHTSDKSTNSSTPPTLTSTKYKIKRYDDGEMPGAPIDKDDNPEFYI 79
DB 1 IYFVKKHTSDKSTNSSTPPTLTSTKYKIKRYDDGEMPGAPIDKDDNPEFYI 60
QY 80 EINLNNIATGFAEMTYNLTSGLVHYVQOLDNIYLRDSNMVHGYPEIFGKPKMNNAY 139
DB 61 EINLNNIATGFAEMTYNLTSGLVHYVQOLDNIYLRDSNMVHGYPEIFGKPKMNNAY 120
QY 140 ATDGPILPSKYSNLTDFLTSTYKLEPKNGLPINFALESWLTREAMRTTGINSDEOEVM 199
DB 121 ATDGPILPSKYSNLTDFLTSTYKLEPKNGLPINFALESWLTREAMRTTGINSDEOEVM 180
QY 200 IWIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIGWEYAFRIKTPKIGETVTI 259
DB 181 IWIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIGWEYAFRIKTPKIGETVTI 240
QY 260 PYGAFISVAANATSSLPNTYELVEVEIGTEGPTSTSAHLEWMTNTITLTPDRPLIS 319
DB 241 PYGAFISVAANATSSLPNTYELVEVEIGTEGPTSTSAHLEWMTNTITLTPDRPLIS 300

RESULT 5

US-10-369-483-3041
Sequence 3041, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B

QY 79 IEINLNNIATGFAEMTYNLTSGLVHYVQOLDNIYLRDSNMVHGYPEIFGKPKMNNAN 138
DB 39 MELNFMNVSXSYG--ETWLKFDGEKVEFADLYNIVLQPSWVGHYEIIYGYKPMAGH 96
QY 139 YATDGPILPSKYSNLTDFLTSTYKLEPKNGLPINFALESWLTREAMRTTGINSDEOEVM 198
DB 97 --NSGVEFLPVAVKOLPDPYTLDSIWENNLPINLMEWTITSPQTS-VSGGDAEI 153
QY 199 MIIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIGWEYAFRIKTPKIGETVT 258
DB 154 MIIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIGWEYAFRIKTPKIGETVT 213
QY 259 IPYGAFTSVANATSSLPNTYELVEVEIGTEGPTSTSAHLEW 303
DB 214 INVQDFVQKAAEVKXKSTRIDNFBELVFCWEIGTEGPTSTSAHLEW 263

Query Match 27.3%; Score 464; DB 15; Length 274;
Best Local Similarity 40.4%; Pred. No. 2.6e-37;
Matches 93; Conservative 43; Mismatches 84; Indels 10; Gaps 4;

QY 79 IEINLNNIATGFAEMTYNLTSGLVHYVQOLDNIYLRDSNMVHGYPEIFGKPKMNNAN 138
DB 39 MELNFMNVSXSYG--ETWLKFDGEKVEFADLYNIVLQPSWVGHYEIIYGYKPMAGH 96
QY 139 YATDGPILPSKYSNLTDFLTSTYKLEPKNGLPINFALESWLTREAMRTTGINSDEOEVM 198
DB 97 --NSGVEFLPVAVKOLPDPYTLDSIWENNLPINLMEWTITSPQTS-VSGGDAEI 153
QY 199 MIIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIGWEYAFRIKTPKIGETVT 258
DB 154 MIIYDGLQDPAGSKYKEIIVPIVNGTPVNATFEVKANIGWEYAFRIKTPKIGETVT 213
QY 259 IPYGAFTSVANATSSLPNTYELVEVEIGTEGPTSTSAHLEW 303
DB 214 INVQDFVQKAAEVKXKSTRIDNFBELVFCWEIGTEGPTSTSAHLEW 263

Query Match 9.8%; Score 166.5; DB 13; Length 261;
Best Local Similarity 26.6%; Pred. No. 7.3e-08;
Matches 66; Conservative 35; Mismatches 108; Indels 39; Gaps 11;

QY 59 DGEWGPAPIDKDDNPEFYI-----NLNMLNNTGFAEMTYNLTSGLVHYV 107
DB 19 DGEWGPAPIDKDDNPEFYI-----NLNMLNNTGFAEMTYNLTSGLVHYV 74
QY 108 QOLDNIVL-----RDSNMVHGYPEIFGKPKMNNAYATDGPILPSKYSNLTDFLTSTY 163
DB 75 -ETGNTTIRADHDGNNNNVAAVPAIYFGH--GACTSNGS--LRRVQELSD--VRSWM 127
QY 164 KLEPKNGLPINFALESWLTREAMRTTGINSDEOEVMWIIYDGLQDPAGSKYKEIIVPI 222
DB 128 TLTPITTGKMAAYDIWSPVTVNSGNGY--SGAELIIMIMNGVMPGSSRVATVEL--- 183